

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Lal, Preeti
Bandman, Olga
- (ii) TITLE OF THE INVENTION: NOVEL HUMAN SODIUM-DEPENDENT
PHOSPHATE COTRANSPORTER
- (iii) NUMBER OF SEQUENCES: 7
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: US
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: Filed Herewith
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Billings, Lucy J.
 - (B) REGISTRATION NUMBER: 36,749
 - (C) REFERENCE/DOCKET NUMBER: PF-0221 US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415-855-0555
 - (B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 401 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: BRAITUT02
 - (B) CLONE: 754412

05991212 11504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Gln Val Asp Glu Thr Leu Ile Pro Arg Lys Val Pro Ser Leu Cys
 1 5 10 15
 Ser Ala Arg Tyr Gly Ile Ala Leu Val Leu His Phe Cys Asn Phe Thr
 20 25 30
 Thr Ile Ala Gln Asn Val Ile Met Asn Ile Thr Met Val Ala Met Val
 35 40 45
 Asn Ser Thr Ser Pro Gln Ser Gln Leu Asn Asp Ser Ser Glu Val Leu
 50 55 60
 Pro Val Asp Ser Phe Gly Gly Leu Ser Lys Ala Pro Lys Ser Leu Pro
 65 70 75 80
 Ala Lys Ser Ser Ile Leu Gly Gly Gln Phe Ala Ile Trp Glu Arg Trp
 85 90 95
 Gly Pro Pro Gln Glu Arg Ser Arg Leu Cys Ser Ile Ala Leu Ser Gly
 100 105 110
 Met Leu Leu Gly Cys Phe Thr Ala Ile Leu Ile Gly Gly Phe Ile Ser
 115 120 125
 Glu Thr Leu Gly Trp Pro Phe Val Phe Tyr Ile Phe Gly Gly Val Gly
 130 135 140
 Cys Val Cys Cys Leu Leu Trp Phe Val Val Ile Tyr Asp Asp Pro Val
 145 150 155 160
 Ser Tyr Pro Trp Ile Ser Thr Ser Glu Lys Glu Tyr Ile Ile Ser Ser
 165 170 175
 Leu Lys Gln Gln Val Gly Ser Ser Lys Gln Pro Leu Pro Ile Lys Ala
 180 185 190
 Met Leu Arg Ser Leu Pro Ile Trp Ser Ile Cys Leu Gly Cys Phe Ser
 195 200 205
 His Gln Trp Leu Val Ser Thr Met Val Val Tyr Ile Pro Thr Tyr Ile
 210 215 220
 Ser Ser Val Tyr His Val Asn Ile Arg Asp Asn Gly Leu Leu Ser Ala
 225 230 235 240
 Leu Pro Phe Ile Val Ala Trp Val Ile Gly Met Val Gly Gly Tyr Leu
 245 250 255
 Ala Asp Phe Leu Leu Thr Lys Lys Phe Arg Leu Ile Thr Val Arg Lys
 260 265 270
 Ile Ala Thr Ile Leu Gly Ser Leu Pro Ser Ser Ala Leu Ile Val Ser
 275 280 285
 Leu Pro Tyr Leu Asn Ser Gly Tyr Ile Thr Ala Thr Ala Leu Leu Thr
 290 295 300
 Leu Ser Cys Gly Leu Ser Thr Leu Cys Gln Ser Gly Ile Tyr Ile Asn
 305 310 315 320
 Val Leu Asp Ile Ala Pro Arg Tyr Ser Ser Phe Leu Met Gly Ala Ser
 325 330 335
 Arg Gly Phe Ser Ser Ile Ala Pro Val Ile Val Pro Thr Val Ser Gly
 340 345 350
 Phe Leu Leu Ser Gln Asp Pro Glu Phe Gly Trp Arg Asn Val Phe Phe
 355 360 365
 Leu Leu Phe Ala Val Asn Leu Leu Gly Leu Leu Phe Tyr Leu Ile Phe
 370 375 380
 Gly Glu Ala Asp Val Gln Glu Trp Ala Lys Glu Arg Lys Leu Thr Arg
 385 390 395 400
 Leu

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1643 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: BRAITUT02
 (B) CLONE: 754412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGAACGGTGA GGATGACCGA CGTATAGGCG AGAGCCTAGG TACGCCATGC CAGGTCACCG 60
 GTCCGGCAAT TCCCGGGTCG ACCCAGCGGT CCGCTTGGAG GGACGCTGGG TTCAACTTGA 120
 AGCCCTTCCA CAGACATTAA GTCGGTGAAA ACCATTCACT AGGAGAGGAG AAACACAATG 180
 GCCACCAAGA CAGAGTTGAG TCCCACAGCA AGGGAGAGCA AGAACGCACA AGATATGCAA 240
 GTGGATGAGA CACTGATCCC CAGGAAAGTT CCAAGTTTAT GTTCTGCTCG CTATGGAATA 300
 GCCCTCGTCT TACATTTCTG CAATTTTACA ACGATAGCAC AAAATGTCAT CATGAACATC 360
 ACCATGGTAG CCATGGTCAA CAGCACAAGC CCTCAATCCC AGCTCAATGA TTCCTCTGAG 420
 GTGCTGCCTG TTGACTCATT TGGTGGCCTA AGTAAAGCCC CAAAGAGTCT TCCTGCAAAG 480
 TCCTCAATAC TTGGGGGTCA GTTTGCAATT TGGGAAAGGT GGGGCCCTCC ACAAGAACGA 540
 AGCAGACTCT GCAGCATTGC TTTATCAGGA ATGTTACTGG GATGCTTTAC TGCCATCCTC 600
 ATAGGTGGCT TCATTAGTGA AACCCTTGGG TGGCCCTTTG TCTTCTATAT CTTTGGAGGT 660
 GTTGGCTGTG TCTGCTGCCT TCTCTGGTTT GTTGTGATTT ATGATGACCC CGTTTCCTAT 720
 CCATGGATAA GCACCTCAGA AAAAGAATAC ATCATATCCT CCTTGAAACA ACAGGTCGGG 780
 TCTTCTAAGC AGCCTCTTCC CATCAAAGCT ATGCTCAGAT CTCTACCCAT TTGGTCCATA 840
 TGTTTAGGCT GTTTCAGCCA TCAATGGTTA GTTAGCACAA TGGTTGTATA CATACCAACT 900
 TACATCAGCT CTGTGTACCA TGTTAACATC AGAGACAATG GACTTCTATC TGCCCTTCCT 960
 TTTATTGTTG CCTGGGTCAT AGGCATGGTG GGAGGCTATC TGGCAGATTT CCTTCTAACC 1020
 AAAAAGTTTA GACTCATCAC TGTGAGGAAA ATTGCCACAA TTTTAGGAAG TCTCCCCTCT 1080
 TCAGCACTCA TTGTGTCTCT GCCTTACCTC AATTCCGGCT ATATCACAGC AACTGCCTTG 1140
 CTGACGCTCT CTTGCGGATT AAGCATATTG TGTCAGTCAG GGATTTATAT CAATGTCTTA 1200
 GATATTGCTC CAAGGTATTC CAGTTTCTCT ATGGGAGCAT CAAGAGGATT TTCGAGCATA 1260
 GCACCTGTCA TTGTACCCAC TGTCAGCGGA TTTCTTCTTA GTCAGGACCC TGAGTTTGGG 1320
 TGGAGGAATG TCTTCTTCTT GCTGTTTGCC GTTAACCTGT TAGGACTACT CTCTACCTC 1380
 ATATTTGGAG AAGCAGATGT CCAAGAATGG GCTAAAGAGA GAAAACTCAC TCGTTTATGA 1440
 AGTTATCCCA CCTTGGATGG AAAAGTCATT AGGCACCGTA TTGCATAAAA TAGAAGGCTT 1500
 CCGTGATGAA AATACCAGTG AAAAGATTTT TTTTTCCTGT GGCTCTTTTC AATTATGAGA 1560
 TCAGTTCATT ATTTTATTCA GACTTTTTTT TGAGAGAAAT GTAAGATGAA TAAAAATTCA 1620
 AATAAAATGA TAACTAAGAA TGC 1643

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 467 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: GenBank
 (B) CLONE: 450532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gln Met Asp Asn Arg Leu Pro Pro Lys Lys Val Pro Gly Phe Cys
 1 5 10 15
 Ser Phe Arg Tyr Gly Leu Ser Phe Leu Val His Cys Cys Asn Val Ile
 20 25 30
 Ile Thr Ala Gln Arg Ala Cys Leu Asn Leu Thr Met Val Val Met Val
 35 40 45

Asn Ser Thr Asp Pro His Gly Leu Pro Asn Thr Ser Thr Lys Lys Leu
 50 55 60
 Leu Asp Asn Ile Lys Asn Pro Met Tyr Asn Trp Ser Pro Asp Ile Gln
 65 70 75 80
 Gly Ile Ile Leu Ser Ser Thr Ser Tyr Gly Val Ile Ile Ile Gln Val
 85 90 95
 Pro Val Gly Tyr Phe Ser Gly Ile Tyr Ser Thr Lys Lys Met Ile Gly
 100 105 110
 Phe Ala Leu Cys Leu Ser Ser Val Leu Ser Leu Leu Ile Pro Pro Ala
 115 120 125
 Ala Gly Ile Gly Val Ala Trp Val Val Val Cys Arg Ala Val Gln Gly
 130 135 140
 Ala Ala Gln Gly Ile Val Ala Thr Ala Gln Phe Glu Ile Tyr Val Lys
 145 150 155 160
 Trp Ala Pro Pro Leu Glu Arg Gly Arg Leu Thr Ser Met Ser Thr Ser
 165 170 175
 Gly Phe Leu Leu Gly Pro Phe Ile Val Leu Leu Val Thr Gly Val Ile
 180 185 190
 Cys Glu Ser Leu Gly Trp Pro Met Val Phe Tyr Ile Phe Gly Ala Cys
 195 200 205
 Gly Cys Ala Val Cys Leu Leu Trp Phe Val Leu Phe Tyr Asp Asp Pro
 210 215 220
 Lys Asp His Pro Cys Ile Ser Ile Ser Glu Lys Glu Tyr Ile Thr Ser
 225 230 235 240
 Ser Leu Val Gln Gln Val Ser Ser Ser Arg Gln Ser Leu Pro Ile Lys
 245 250 255
 Ala Ile Leu Lys Ser Leu Pro Val Trp Ala Ile Ser Ile Gly Ser Phe
 260 265 270
 Thr Phe Phe Trp Ser His Asn Ile Met Thr Leu Tyr Thr Pro Met Phe
 275 280 285
 Ile Asn Ser Met Leu His Val Asn Ile Lys Glu Asn Gly Phe Leu Ser
 290 295 300
 Ser Leu Pro Tyr Leu Phe Ala Trp Ile Cys Gly Asn Leu Ala Gly Gln
 305 310 315 320
 Leu Ser Asp Phe Phe Leu Thr Arg Asn Ile Leu Ser Val Ile Ala Val
 325 330 335
 Arg Lys Leu Phe Thr Ala Ala Gly Phe Leu Leu Pro Ala Ile Phe Gly
 340 345 350
 Val Cys Leu Pro Tyr Leu Ser Ser Thr Phe Tyr Ser Ile Val Ile Phe
 355 360 365
 Leu Ile Leu Ala Gly Ala Thr Gly Ser Phe Cys Leu Gly Gly Val Phe
 370 375 380
 Ile Asn Gly Leu Asp Ile Ala Pro Arg Tyr Phe Gly Phe Ile Lys Ala
 385 390 395 400
 Cys Ser Thr Leu Thr Gly Met Ile Gly Gly Leu Ile Ala Ser Thr Leu
 405 410 415
 Thr Gly Leu Ile Leu Lys Gln Asp Pro Glu Ser Ala Trp Phe Lys Thr
 420 425 430
 Phe Ile Leu Met Ala Ala Ile Asn Val Thr Gly Leu Ile Phe Tyr Leu
 435 440 445
 Ile Val Ala Thr Ala Glu Ile Gln Asp Trp Ala Lys Glu Lys Gln His
 450 455 460
 Thr Arg Leu
 465

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 560 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank
 (B) CLONE: 507415

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Glu	Phe	Arg	Gln	Glu	Glu	Phe	Arg	Lys	Leu	Ala	Gly	Arg	Ala	Leu
1				5					10					15	
Gly	Arg	Leu	His	Arg	Leu	Leu	Glu	Lys	Arg	Gln	Glu	Gly	Ala	Glu	Thr
			20					25					30		
Leu	Glu	Leu	Ser	Ala	Asp	Gly	Arg	Pro	Val	Thr	Thr	His	Thr	Arg	Asp
		35					40					45			
Pro	Pro	Val	Val	Asp	Cys	Thr	Cys	Phe	Gly	Leu	Pro	Arg	Arg	Tyr	Ile
	50				55						60				
Ile	Ala	Ile	Met	Ser	Gly	Leu	Gly	Phe	Cys	Ile	Ser	Phe	Gly	Ile	Arg
65					70					75				80	
Cys	Asn	Leu	Gly	Val	Ala	Ile	Val	Ser	Met	Val	Asn	Asn	Ser	Thr	Thr
			85						90					95	
His	Arg	Gly	Gly	His	Val	Val	Val	Gln	Lys	Ala	Gln	Phe	Asn	Trp	Asp
			100					105					110		
Pro	Glu	Thr	Val	Gly	Leu	Ile	His	Gly	Ser	Phe	Phe	Trp	Gly	Tyr	Ile
	115						120					125			
Val	Thr	Gln	Ile	Pro	Gly	Gly	Phe	Ile	Cys	Gln	Lys	Phe	Ala	Ala	Asn
	130					135					140				
Arg	Val	Phe	Gly	Phe	Ala	Ile	Val	Ala	Thr	Ser	Thr	Leu	Asn	Met	Leu
145					150					155					160
Ile	Pro	Ser	Ala	Ala	Arg	Val	His	Tyr	Gly	Cys	Val	Ile	Phe	Val	Arg
			165						170					175	
Ile	Leu	Gln	Gly	Leu	Val	Glu	Gly	Val	Thr	Tyr	Pro	Ala	Cys	His	Gly
		180					185					190			
Ile	Trp	Ser	Lys	Trp	Ala	Pro	Pro	Leu	Glu	Arg	Ser	Arg	Leu	Ala	Thr
	195					200						205			
Thr	Ala	Phe	Cys	Gly	Ser	Tyr	Ala	Gly	Ala	Val	Val	Ala	Met	Pro	Leu
	210					215					220				
Ala	Gly	Val	Leu	Val	Gln	Tyr	Ser	Gly	Trp	Ser	Ser	Val	Phe	Tyr	Val
225					230				235						240
Tyr	Gly	Ser	Phe	Gly	Ile	Phe	Trp	Tyr	Leu	Phe	Trp	Leu	Leu	Val	Ser
			245						250					255	
Tyr	Glu	Ser	Pro	Ala	Leu	His	Pro	Ser	Ile	Ser	Glu	Glu	Glu	Arg	Lys
		260						265					270		
Tyr	Ile	Glu	Asp	Ala	Ile	Gly	Glu	Ser	Ala	Lys	Leu	Met	Asn	Pro	Val
	275					280						285			
Thr	Lys	Phe	Asn	Thr	Pro	Trp	Arg	Arg	Phe	Phe	Thr	Ser	Met	Pro	Val
	290					295					300				
Tyr	Ala	Ile	Ile	Val	Ala	Asn	Phe	Cys	Arg	Ser	Trp	Thr	Phe	Tyr	Leu
305					310					315					320
Leu	Leu	Ile	Ser	Gln	Pro	Ala	Tyr	Phe	Glu	Glu	Val	Phe	Gly	Phe	Glu
			325						330					335	
Ile	Ser	Lys	Val	Gly	Leu	Val	Ser	Ala	Leu	Pro	His	Leu	Val	Met	Thr
		340						345					350		
Ile	Ile	Val	Pro	Ile	Gly	Gly	Gln	Ile	Ala	Asp	Phe	Leu	Arg	Ser	Arg
		355				360						365			
His	Ile	Met	Ser	Thr	Thr	Asn	Val	Arg	Lys	Leu	Met	Asn	Cys	Gly	Gly
	370					375					380				
Phe	Gly	Met	Glu	Ala	Thr	Leu	Leu	Leu	Val	Val	Gly	Tyr	Ser	His	Ser

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385 390 395 400
 Lys Gly Val Ala Ile Ser Phe Leu Val Leu Ala Val Gly Phe Ser Gly
 405 410 415
 Phe Ala Ile Ser Gly Phe Asn Val Asn His Leu Asp Ile Ala Pro Arg
 420 425 430
 Tyr Ala Ser Ile Leu Met Gly Ile Ser Asn Gly Val Gly Thr Leu Ser
 435 440 445
 Gly Met Val Cys Pro Ile Ile Val Gly Ala Met Thr Lys His Lys Thr
 450 455 460
 Arg Glu Glu Trp Gln Tyr Val Phe Leu Ile Ala Ser Leu Val His Tyr
 465 470 475 480
 Gly Gly Val Ile Phe Tyr Gly Val Phe Ala Ser Gly Glu Lys Gln Pro
 485 490 495
 Trp Ala Glu Pro Glu Glu Met Ser Glu Glu Lys Cys Gly Phe Val Gly
 500 505 510
 His Asp Gln Leu Ala Gly Ser Asp Glu Ser Glu Met Glu Asp Glu Val
 515 520 525
 Glu Pro Pro Gly Ala Pro Pro Ala Pro Pro Pro Ser Tyr Gly Ala Thr
 530 535 540
 His Ser Thr Val Gln Pro Pro Arg Pro Pro Pro Pro Val Arg Asp Tyr
 545 550 555 560

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAITUT02
- (B) CLONE: 754412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATTTATATCA ATGTCTTAGA TATTGCTCCA AGGTATTCCA GTTTTCTCAT GGGAGCATCA 60
 AGAGGATTTT CGAGCATAGC ACCTGTCATT GTACCCACTG TCAGTGGATT TCTTCTTAGT 120
 CAGGACCCTG AGTTTGGGTG GAGGAATGTC TTCTTCTTGC TGTTTGCCGT TAACCTGTTA 180
 GGACTACTCT TCTACCTCAT ATTTGGAGAA GCAGATGTCC AAGAATGGGC TAAAGAGAGA 240
 AAACACTCTC GTTTATGAAG TTATCCCACC TT 272

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (B) CLONE: XLR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTTGATGCTC CCATGAGAAA ACTGG 25

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (B) CLONE: XLF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AGGATTTTCG AGCATAGCAC CTGTC

25

09991212 11501